

71264

LB

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From: Davis, Minh-Tam
Sent: Thursday, July 18, 2002 9:53 AM
To: STIC-Biotech/ChemLib
Subject: Search request for 09/840746

Please search in commercial database and in issued patent files:

1) SEQ ID NOs: 1 and 2

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MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

priority date
4/01

Point of Contact
P. Sheppard
Telephone number: (703) 308-4499

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 7/26/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 25, 2002, 19:34:16 ; Search time 12075.4 Seconds
(without alignments)
12047.710 Million cell updates/sec

Title: US-09-840-746-2

Perfect score: 6952
Sequence: 1 gtcgagtaaaagaattgccg.....tactggaagctataggtg 6952

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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29: em_vl: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

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| 1 | 5140.4 | 73.9 | 5142 | 9 | AB033063 | AB033063 Homo sapi |
| 2 | 5098.4 | 73.3 | 6407 | 6 | AR065869 | AR065869 Sequence |
| 3 | 3508.6 | 50.5 | 189933 | 2 | AC026342 | AC026342 Homo sapi |
| 4 | 3500.6 | 50.4 | 110000 | 2 | AC092983-0 | AC092983 Homo sapi |
| 5 | 1438.8 | 20.7 | 1462 | 9 | BC004539 | BC004539 Homo sapi |
| 6 | 1384.8 | 19.9 | 1397 | 9 | BC014053 | BC014053 Homo sapi |
| 7 | 1359.8 | 19.6 | 110000 | 2 | AC092983-0 | AC092983 Homo sapi |
| 8 | 663 | 9.5 | 118407 | 2 | AC026629 | AC026629 Homo sapi |
| 9 | 610.8 | 8.8 | 118407 | 2 | AC026629 | AC026629 Homo sapi |
| 10 | 387.4 | 5.6 | 400 | 6 | AX245407 | AX245407 Sequence |
| 11 | 326.2 | 4.7 | 50921 | 2 | AC092983-3 | AC092983 Homo sapi |
| 12 | 266.4 | 3.8 | 115766 | 2 | AC069571 | AC069571 Homo sapi |
| 13 | 263.4 | 3.8 | 34308 | 9 | AF389852 | AF389852 Homo sapi |
| 14 | 126.4 | 1.8 | 128 | 6 | AR053542 | AR053542 Homo sapi |
| 15 | 126.4 | 1.8 | 128 | 6 | AR080351 | AR080351 Sequence |
| 16 | 126.4 | 1.8 | 128 | 6 | AR148306 | AR148306 Sequence |
| 17 | 112 | 1.6 | 112 | 11 | G20489 | G20489 human STR A |
| 18 | 102.6 | 1.5 | 2008 | 9 | AB062989 | AB062989 Macaca fa |
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| 21 | 67.6 | 1.0 | 150110 | 2 | AC097722 | AC097722 Homo sapi |
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| 37 | 62.4 | 0.9 | 126736 | 2 | AC044788 | AC044788 Homo sapi |
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| 44 | 61.8 | 0.9 | 146438 | 9 | HSBA19119 | AL17329 Human DNA |
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ALIGNMENTS

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LOCUS AB033063
DEFINITION Homo sapiens mRNA for KIAA1237 protein, partial cds.
ACCESSION AB033063
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens brain cDNA to mRNA, clone_11b:pb1uescriptII SK plus
clone:fh09696.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Nagase,T., Ishikawa,K., Kikuno,R., Hirotsawa,M., Nomura,N. and
Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes. XV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro
JOURNAL DNA Res. 6 (5), 337-345 (1999)
MEDLINE 2 (bases 1 to 5142)
REFERENCE Ohara,O., Nagase,T. and Kikuno,R.
AUTHORS
TITLE Direct Submission

OM nucleic - nucleic search, using sw model

Run on: July 25, 2002, 20:03:31 ; Search time 192.67 Seconds
(without alignments)
8863.051 Million cell updates/sec

Title: US-09-840-746-2
Perfect score: 6952
Sequence: 1 gttcgtatgaagaattgccc.....tactgggaactataggtg 6952

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
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| 1 | 5098.4 | 73.3 | 6407 | 2 | US-08-616-844-7 |
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| 3 | 5098.4 | 73.3 | 6407 | 3 | US-08-944-868A-7 |
| 4 | 5098.4 | 73.3 | 6407 | 3 | US-08-944-868A-7 |
| 5 | 5098.4 | 73.3 | 6407 | 3 | US-08-944-423A-7 |
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| 7 | 126.4 | 1.8 | 128 | 2 | US-08-480-994-7 |
| 8 | 126.4 | 1.8 | 128 | 2 | US-08-485-573-7 |
| 9 | 126.4 | 1.8 | 128 | 2 | US-08-925-743-7 |
| 10 | 126.4 | 1.8 | 128 | 4 | US-08-925-767-7 |
| 11 | 89.8 | 1.3 | 7218 | 1 | US-08-232-463-14 |
| 12 | 56.2 | 0.8 | 3489 | 1 | US-08-728-323A-1 |
| 13 | 56.2 | 0.8 | 32207 | 2 | US-08-770-379-20 |
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| 15 | 56.2 | 0.8 | 32207 | 4 | US-09-230-371A-20 |
| 16 | 52.8 | 0.8 | 2518 | 4 | US-09-433-699-3 |
| 17 | 49.4 | 0.7 | 1236 | 4 | US-08-741-134-5 |
| 18 | 48.8 | 0.7 | 289 | 4 | US-09-007-005-17 |
| 19 | 48.8 | 0.7 | 289 | 4 | US-09-244-796-17 |
| 20 | 48.8 | 0.7 | 696 | 4 | US-09-461-697-193 |
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| 22 | 48.8 | 0.7 | 717 | 4 | US-09-461-697-189 |
| 23 | 48.8 | 0.7 | 774 | 4 | US-09-461-697-187 |
| 24 | 48.8 | 0.7 | 819 | 4 | US-09-461-697-185 |
| 25 | 48.6 | 0.7 | 1659 | 4 | US-09-461-697-184 |
| 26 | 48.6 | 0.7 | 1931 | 2 | US-09-130-114-2 |
| 27 | 48.2 | 0.7 | 966 | 2 | US-08-766-738-2 |

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| 28 | 48.2 | 0.7 | 3211 | 4 | US-08-574-959A-8 | Sequence 8, Appl1 |
| 29 | 48.2 | 0.7 | 3211 | 4 | US-09-357-014-8 | Sequence 8, Appl1 |
| 30 | 48.2 | 0.7 | 3901 | 2 | US-08-574-959A-6 | Sequence 6, Appl1 |
| 31 | 48.2 | 0.7 | 3901 | 4 | US-09-357-014-6 | Sequence 6, Appl1 |
| 32 | 46.6 | 0.7 | 1052 | 1 | US-08-466-603-1 | Sequence 1, Appl1 |
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| 34 | 46.6 | 0.7 | 1052 | 1 | US-08-468-065-1 | Sequence 1, Appl1 |
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| 36 | 46.6 | 0.7 | 1052 | 3 | US-08-466-743-1 | Sequence 1, Appl1 |
| 37 | 46.6 | 0.7 | 1052 | 5 | PCT-US95-12414-1 | Sequence 1, Appl1 |
| 38 | 46.6 | 0.7 | 18596 | 4 | US-09-318-448-11 | Sequence 1, Appl1 |
| 39 | 44.8 | 0.6 | 9636 | 1 | US-08-323-170B-1 | Sequence 1, Appl1 |
| 40 | 44.8 | 0.6 | 9636 | 4 | US-08-954-441-1 | Sequence 1, Appl1 |
| 41 | 44.2 | 0.6 | 5163 | 3 | US-08-700-651-1 | Sequence 1, Appl1 |
| 42 | 44.2 | 0.6 | 5163 | 3 | US-08-928-361B-4 | Sequence 1, Appl1 |
| 43 | 44.2 | 0.6 | 5318 | 3 | US-08-700-651-2 | Sequence 2, Appl1 |
| 44 | 44.2 | 0.6 | 5318 | 3 | US-08-928-361B-3 | Sequence 3, Appl1 |
| 45 | 43.6 | 0.6 | 43795 | 3 | US-08-742-185-101 | Sequence 101, App |

ALIGNMENTS

RESULT 1
US-08-616-844-7
Sequence 7, Application US/08616844
Patent No. 5849578
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,844
FILING DATE: 15-MAR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6407 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
US-08-616-844-7

[illegible]

RESULT 2
 ; Sequence 7, Application US/08599654
 ; Patent No. 5882925
 ; GENERAL INFORMATION:
 ; APPLICANT: FALB, DEAN A
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PENNIE & EDMONDS
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/599,654
 ; FILING DATE: 09-FEB-1996
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,573
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/386,844
 ; FILING DATE: 10-FEB-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CORUZZI, LAURA A
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-041
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6407 base-pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: CDNA
 ;

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OM nucleic - nucleic search, using sw model

Run on: July 25, 2002, 19:34:16 ; Search time 12075.4 Seconds

(without alignments)
12047.710 Million cell updates/sec

Title: US-09-840-746-2

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Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_da: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 5098.4 | 73.3 | 6407 | 6 | AR065869 | AR065869 Sequence |
| 3 | 3508.6 | 50.5 | 189933 | 2 | AC026342 | AC026342 Homo sapi |
| 4 | 3500.6 | 50.4 | 110000 | 2 | AC092983_0 | AC092983 Homo sapi |
| 5 | 1438.8 | 20.7 | 1462 | 9 | BC004539 | BC004539 Homo sapi |
| 6 | 1384.8 | 19.9 | 1397 | 9 | BC014053 | BC014053 Homo sapi |
| 7 | 1359.8 | 19.6 | 110000 | 2 | AC092983_0 | AC092983 Homo sapi |
| 8 | 663 | 9.5 | 118407 | 2 | AC026629 | AC026629 Homo sapi |
| 9 | 610.8 | 8.8 | 118407 | 2 | AC026629 | AC026629 Homo sapi |
| 10 | 387.4 | 5.6 | 4400 | 6 | AX245407 | AX245407 Homo sapi |
| 11 | 326.2 | 4.7 | 50921 | 2 | AC092983_3 | AC092983_3 Sequence |
| 12 | 266.4 | 3.8 | 115766 | 2 | AC069571 | AC069571 Homo sapi |
| 13 | 263.4 | 3.8 | 34308 | 9 | AF389852 | AF389852 Homo sapi |
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| 15 | 126.4 | 1.8 | 128 | 6 | AR080351 | AR080351 Sequence |
| 16 | 126.4 | 1.8 | 128 | 6 | AR148306 | AR148306 Sequence |
| 17 | 112 | 1.6 | 112 | 11 | G20489 | G20489 human STS A |
| 18 | 102.6 | 1.5 | 2008 | 9 | AB062989 | AB062989 Macaca fa |
| 19 | 89.8 | 1.3 | 7218 | 6 | 166494 | 166494 Sequence (3 of |
| 20 | 88 | 1.3 | 110000 | 2 | AC092983_2 | AC092983_2 Homo sapi |
| 21 | 67.6 | 1.0 | 150110 | 2 | AC097722 | AC097722 Homo sapi |
| 22 | 67.6 | 1.0 | 177475 | 2 | AL626782 | AL626782 Mus muscu |
| 23 | 67 | 1.0 | 179282 | 2 | AC079507 | AC079507 Mus muscu |
| 24 | 65.8 | 0.9 | 2384 | 3 | PFAGAR | J03998 Plasmodium |
| 25 | 65.6 | 0.9 | 397 | 11 | G37798 | G37798 GARP plasm |
| 26 | 65.2 | 0.9 | 56757 | 2 | AC105856 | AC105856 Rattus no |
| 27 | 64.8 | 0.9 | 174591 | 2 | AC103093 | AC103093 Rattus no |
| 28 | 64.4 | 0.9 | 197844 | 2 | AC079176 | AC079176 Homo sapi |
| 29 | 63.6 | 0.9 | 156224 | 2 | AC096059 | AC096059 Rattus no |
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| 31 | 63.4 | 0.9 | 91999 | 2 | AC095962 | AC095962 Rattus no |
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| 33 | 63 | 0.9 | 194472 | 2 | AC096438 | AC096438 Rattus no |
| 34 | 62.8 | 0.9 | 166704 | 2 | AC078821 | AC078821 Homo sapi |
| 35 | 62.6 | 0.9 | 184855 | 2 | AL606744 | AL606744 Mus muscu |
| 36 | 62.6 | 0.9 | 209671 | 10 | AC096777 | AC096777 Mus muscu |
| 37 | 62.4 | 0.9 | 126736 | 2 | AC044788 | AC044788 Homo sapi |
| 38 | 62.4 | 0.9 | 182288 | 9 | AC018362 | AC018362 Homo sapi |
| 39 | 62.4 | 0.9 | 203298 | 2 | AP001178 | AP001178 Homo sapi |
| 40 | 62.4 | 0.9 | 244490 | 2 | AC105495 | AC105495 Rattus no |
| 41 | 62.2 | 0.9 | 82973 | 2 | AC105453 | AC105453 Rattus no |
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| 43 | 62 | 0.9 | 202904 | 2 | AL603837 | AL603837 Mus muscu |
| 44 | 61.8 | 0.9 | 146438 | 9 | HSBA19119 | AL117329 Human DNA |
| 45 | 61.6 | 0.9 | 174990 | 10 | AC027653 | AC027653 Mus muscu |

ALIGNMENTS

RESULT 1
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DEFINITION AB033063
ACCESSION AB033063
VERSION
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (sites) Nagase, T., Ishikawa, K., Kikuno, R., Hirosewa, M., Nomura, N. and Ohara, O.
Prediction of the coding sequences of unidentified human genes. XV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro
DNA Res. 6 (5), 337-345 (1999)
JOURNAL 2 (bases 1 to 5142)
MEDLINE
REFERENCE
AUTHORS Ohara, O., Nagase, T. and Kikuno, R.
TITLE Direct Submission

JOURNAL Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdna@ohara.kazusa.or.jp, URL: http://www.kazusa.or.jp/huge/, Tel: +81-438-52-3913, Fax: +81-438-52-3914)

FEATURES

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| AUTHORS | 1 (bases 1 to 6407) | | |
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| FEATURES | cardiovascular using RCHD528 as a target | | |
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3: /cgn2_6/ptodata/2/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCRTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|---------------------|---------------------|
| 1 | 5098.4 | 73.3 | 6407 | 2 US-08-616-844-7 | Sequence 7, Appl 1 |
| 2 | 5098.4 | 73.3 | 6407 | 2 US-08-599-654-7 | Sequence 7, Appl 1 |
| 3 | 5098.4 | 73.3 | 6407 | 3 US-08-944-868A-7 | Sequence 7, Appl 1 |
| 4 | 5098.4 | 73.3 | 6407 | 3 US-08-944-823A-7 | Sequence 7, Appl 1 |
| 5 | 5098.4 | 73.3 | 6407 | 3 US-08-944-496-7 | Sequence 7, Appl 1 |
| 6 | 470.4 | 6.8 | 584 | 4 US-09-328-111-83 | Sequence 83, Appl 1 |
| 7 | 126.4 | 1.8 | 128 | 2 US-08-480-994-7 | Sequence 7, Appl 1 |
| 8 | 126.4 | 1.8 | 128 | 2 US-08-485-573-7 | Sequence 7, Appl 1 |
| 9 | 126.4 | 1.8 | 128 | 3 US-08-925-743-7 | Sequence 7, Appl 1 |
| 10 | 126.4 | 1.8 | 128 | 3 US-08-925-767-7 | Sequence 7, Appl 1 |
| 11 | 89.8 | 1.3 | 7218 | 1 US-08-232-463-14 | Sequence 14, Appl 1 |
| 12 | 56.2 | 0.8 | 3489 | 2 US-08-728-323A-1 | Sequence 1, Appl 1 |
| 13 | 56.2 | 0.8 | 32207 | 2 US-08-770-379-20 | Sequence 20, Appl 1 |
| 14 | 56.2 | 0.8 | 32207 | 2 US-08-757-669A-20 | Sequence 20, Appl 1 |
| 15 | 56.2 | 0.8 | 32207 | 4 US-09-230-371A-20 | Sequence 3, Appl 1 |
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| 17 | 49.4 | 0.7 | 1236 | 2 US-08-741-134-5 | Sequence 17, Appl 1 |
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| 19 | 48.8 | 0.7 | 289 | 4 US-09-244-796-17 | Sequence 19, Appl 1 |
| 20 | 48.8 | 0.7 | 696 | 4 US-09-461-697-193 | Sequence 19, Appl 1 |
| 21 | 48.8 | 0.7 | 699 | 4 US-09-461-697-191 | Sequence 189, App |
| 22 | 48.8 | 0.7 | 717 | 4 US-09-461-697-189 | Sequence 187, App |
| 23 | 48.8 | 0.7 | 774 | 4 US-09-461-697-187 | Sequence 185, App |
| 24 | 48.8 | 0.7 | 819 | 4 US-09-461-697-185 | Sequence 184, App |
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| 27 | 48.2 | 0.7 | 966 | 2 US-08-766-738-2 | Sequence 2, Appl 1 |

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| 28 | 48.2 | 0.7 | 3211 | 2 US-08-574-959A-8 | Sequence 8, Appl 1 |
| 29 | 48.2 | 0.7 | 3211 | 4 US-09-357-014-8 | Sequence 8, Appl 1 |
| 30 | 48.2 | 0.7 | 3901 | 2 US-08-574-959A-6 | Sequence 6, Appl 1 |
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| 32 | 46.6 | 0.7 | 1052 | 1 US-08-466-603-1 | Sequence 1, Appl 1 |
| 33 | 46.6 | 0.7 | 1052 | 1 US-08-314-503A-1 | Sequence 1, Appl 1 |
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| 36 | 46.6 | 0.7 | 1052 | 2 US-08-466-743-1 | Sequence 1, Appl 1 |
| 37 | 46.6 | 0.7 | 1052 | 5 PCT-US95-12414-1 | Sequence 11, Appl 1 |
| 38 | 46.6 | 0.7 | 18596 | 4 US-09-318-448-11 | Sequence 1, Appl 1 |
| 39 | 44.8 | 0.6 | 9636 | 1 US-08-323-170B-1 | Sequence 1, Appl 1 |
| 40 | 44.8 | 0.6 | 9636 | 4 US-08-954-441-1 | Sequence 1, Appl 1 |
| 41 | 44.2 | 0.6 | 5163 | 3 US-08-700-651-4 | Sequence 1, Appl 1 |
| 42 | 44.2 | 0.6 | 5163 | 3 US-08-928-361B-4 | Sequence 2, Appl 1 |
| 43 | 44.2 | 0.6 | 5318 | 3 US-08-700-651-2 | Sequence 3, Appl 1 |
| 44 | 44.2 | 0.6 | 5318 | 3 US-08-928-361B-3 | Sequence 101, App |
| 45 | 43.6 | 0.6 | 43795 | 3 US-08-742-185-101 | |

ALIGNMENTS

RESULT 1
US-08-616-844-7
Sequence 7, Application US/08616844
Patent No. 5849578

GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESS: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,844
FILING DATE: 15-MAR-1996
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
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TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6407 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
US-08-616-844-7

| | | | |
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| OY | 2940 | cyttgcctctgycacagtgcaagtcgysga tacttcaagtlccaaacaaga tggacaactctg | 2999 |
| Db | 3906 | CGTTGCCCTGTGCCAGTGGCAAGTCGGGATTACTTTCAGTCAACAAGATGGACCACTCTCTG | 3966 |
| OY | 3000 | cagagcatgtgaagatgatatgaagcttgaaatgaaacctgcatagagttggccatttgg | 3055 |
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| OY | 3060 | cccttgatgtctccaactgtgaaacctatccaactataactctgtgtgtatctgcagccgc | 3111 |
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| OY | 3360 | aaggaatccagaacttgaaegaaacggaacttaccgcgcctacactgysgaatgcagaatc | 3411 |
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| OY | 3600 | gctgagctggcgaagcaagaagaagagcaatgcgysgcgtgcaccaagtgysgaagagaca | 3655 |
| Db | 4566 | GCTGATGTGCAAGCAGAGAAAGGAGACAGGCATTCGGGGCTGTACACACAGTGGAGGAGACA | 4622 |
| OY | 3660 | ggtgagctgtgaaccacaagcgtgctaatatgaacacttggttgttctacgttgaactgaaat | 3711 |
| Db | 4626 | GGTGATGTGGAAACCAACAGGCTGCTCATTTAGACACTTTGTTTGTATCTGTGAACGTGAAT | 4688 |
| OY | 3720 | gtgggcagatcaacaagagatctctctgagtgactgcacatatgysacttgcgaccaagysg | 3777 |
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| Db | 4746 | ACTATTAGCCAGGCAAGACCACTAAGATTCAGTGACGAGGAGACCTCGTTTCCCTTCTGTTTG | 4800 |
| OY | 3840 | caacttgatgaatttgggtgysgaagtttccctttgatactgttlttgagactgttccagaaa | 3899 |
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| OY | 3960 | aatactgctgttgaattatatttccctgcgccaagcgcctgcgtctaaacaagaatgysga | 4019 |

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